WHAT IS CLAIMED IS:

1. A method of detecting cancer in a patient, the method comprising:

determining the level of a transcript encoding SEQ ID NO:2 in a biological sample from the patient; and

detecting a decrease in the level of the transcript relative to normal, thereby detecting the presence of cancer in the patient.

2. The method of claim 1, wherein the cancer is selected from a group consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.

3. The method of claim 1, wherein the step of determining the level of the transcript comprises an amplification reaction.

4. A method of detecting cancer in a patient, the method comprising:

determining the level of a polypeptide having the sequence set forth in SEQ ID NO:2 in a biological sample from the patient: and

detecting an increase in the level of the polypeptide relative to normal, thereby detecting the presence of cancer in the patient.

5. The method of claim 4, wherein the cancer is selected from the group consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.

6. The method of claim 4, wherein the step of determining the level of the polypeptide comprises performing an immunoassay.

7. A method of detecting cancer in a patient, the method comprising:

determining the amount of methylation of a SOCS-3 promoter in a biological sample from the patient; and

detecting an increase in the amount of methylation of the sample relative to normal, thereby detecting the presence of cancer in the patient.

8. The method of claim 7, wherein the amount of methylation of the CpG residues that occur within the region from -1005 to -983 or from -754 to -737 of SEQ ID NO:3 is determined.

9. The method of claim 7, wherein the amount of methylation of the SOCS-3 promoter is determined using bisulfite sequencing.

10. The method of claim 7, wherein the amount of methylation of the SOCS-3 promoter is determined using methylation-specific PCR.

11. The method of claim 7, wherein the amount of methylation is detected using a methylation-sensitive restriction enzyme.

12. A method of monitoring the efficacy of a therapeutic treatment of cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) detecting the level of: a polypeptide having an amino acid sequence of SEQ ID NO:2, or of a nucleic acid that encodes the polypeptide, in the biological sample compared to a level in a biological sample from the patient prior to, or earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

13. A method of monitoring the efficacy of a therapeutic treatment of cancer, the method comprising the steps of:

(i) providing a biological sample from a patient undergoing the therapeutic treatment; and

(ii) detecting the level of methylation of the SOCS-3 promoter in the biological sample compared to a level in a biological sample from the patient prior to, or earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

14. A method of screening for an agent that increases SOCS-3 activity, the method comprising

incubating a test compound with a cell comprising a SOCS-3 nucleic acid having at least 80% identity to SEQ ID NO:1;

selecting a compound that increases SOCS-3 activity, thereby identifying an agent that increases SOCS-3 activity.

15. The method of claim 14, wherein the SOCS-3 nucleic acid sequence further comprises a hypermethylated promoter.

16. The method of claim 15, further comprising a step of determining the amount of methylation of the SOCS-3 promoter following incubation with the test compound.

17. The method of claim 14, wherein the increase in SOCS-3 activity is determined by measuring the level of SOCS-3 mRNA transcript.

18. The method of claim 14, wherein the increase in SOCS-3 activity is determined by measuring the level of SOCS-3 polypeptide.

19. A method of inhibiting proliferation of a cancer cell, the method comprising administering an agent that increases SOCS-3 activity to the cancer cell.

20. The method of claim 19, wherein the cancer cell has a hypermethylated SOCS-3 promoter.

21. The method of claim 20, wherein the cancer cell is selected from the group consisting of a lung cancer cell, a breast cancer cell, a mesothelioma cell, a colon cancer cell, and a sarcoma cell.

22. The method of claim 19, wherein the agent is an expression vector encoding SOCS-3.

23. The method of claim 19, wherein the agent is recombinant SOCS-3.

24. The method of claim 19, wherein the agent is a demethylating agent.

25. A kit comprising methylation-specific primers that are selective for methylated residues present within the region from -1005 to -983 or from -754 to -737 of SEQ ID NO:3.